We claim:

1. A method of identifying a preferred liver transplant donor, comprising determining in an individual the presence or absence of a preferred genotype at a polymorphic site, said preferred genotype associated with altered activity of a tumor necrosis factor, wherein the presence of said preferred genotype indicates that said individual is a preferred liver transplant donor.

2. The method of claim 1, further comprising reporting the presence or absence of said preferred genotype.

3. The method of claim 1, wherein said preferred genotype is associated with lower activity of said tumor necrosis factor.

4. The method of claim 3, wherein said tumor necrosis factor is TNF-α.

5. The method of claim 3, wherein said preferred genotype is associated with lower levels of said tumor necrosis factor.

6. The method of claim 5, wherein said tumor necrosis factor is TNF-α.

7. The method of claim 6, wherein said preferred genotype is TNF308.1.

8. The method of claim 1, wherein said polymorphic site is in a TNF-α regulatory region.

9. The method of claim 8, wherein said polymorphic site is in a TNF-α transcriptional regulatory region.

10. The method of claim 9, wherein said polymorphic site is in a TNF-α promoter region.

11. The method of claim 1, wherein said polymorphic site is in a TNF-α coding region.

12. The method of claim 1, wherein said liver transplant donor is identified for transplantation into a hepatitis C virus infected patient.

13. A method for selecting a preferred liver for transplantation, comprising the steps of:

(a) obtaining material from one or more potential liver donors;

(b) determining in said one or more potential liver donors the presence or absence of a preferred genotype at a polymorphic site, said preferred genotype associated with altered activity of a tumor necrosis factor; and

(c) harvesting a liver, or functional portion thereof, having a preferred genotype.

14. The method of claim 13, further comprising the step of:

(d) transplanting said liver, or functional portion thereof, into a recipient.

15. The method of claim 13, wherein said preferred genotype is associated with lower activity of said tumor necrosis factor.

16. The method of claim 15, wherein said tumor necrosis factor is TNF-α.

17. The method of claim 15, wherein said preferred genotype is associated with lower levels of said tumor necrosis factor.

18. The method of claim 17, wherein said tumor necrosis factor is TNF-α.

19. The method of claim 18, wherein said preferred genotype is TNF308.1.

20. The method of claim 13, wherein said polymorphic site is in a TNF-α regulatory region.

21. The method of claim 20, wherein said polymorphic site is in a TNF-α transcriptional regulatory region.

22. The method of claim 21, wherein said polymorphic site is in a TNF-α promoter region.

23. The method of claim 13, wherein said polymorphic site is in a TNF-α coding region.

24. The method of claim 14, wherein said recipient is infected with hepatitis C virus.

25. A method for limiting the severity of recurrence of hepatitis C in a liver transplant recipient, comprising the steps of:

(a) obtaining material from one or more potential liver donors;

(b) determining in said one or more potential liver donors the presence or absence of a preferred genotype at a polymorphic site, said preferred genotype associated with altered activity of a tumor necrosis factor;

(c) harvesting a liver, or functional portion thereof, having a preferred genotype; and

(d) transplanting said liver, or functional portion thereof, into a recipient infected with hepatitis C virus.

26. The method of claim 25, wherein said preferred genotype is associated with lower activity of said tumor necrosis factor.

27. The method of claim 26, wherein said tumor necrosis factor is TNF-α.

28. The method of claim 26, wherein said preferred genotype is associated with lower levels of said tumor necrosis factor.

29. The method of claim 28, wherein said tumor necrosis factor is TNF-α.

30. The method of claim 29, wherein said preferred genotype is TNF308.1.

31. The method of claim 25, wherein said polymorphic site is in a TNF-α regulatory region.

32. The method of claim 31, wherein said polymorphic site is in a TNF-α transcriptional regulatory region.

33. The method of claim 32, wherein said polymorphic site is in a TNF-α promoter region.

34. The method of claim 25, wherein said polymorphic site is in a TNF-α coding region.